

HGRA4sv.cds	(1)	1	50
SEQ ID NO:23	(1)	ATGACAACCTCTTGTTCCTGCAACCCTCTCCTTCCTTCTTCTCTGGACCT	

HGRA4sv.cds	(51)	51	100
SEQ ID NO:23	(1)	GCCAGGGCAGGTCTCTCTCAAGGGTGGCCTTGGCAAAGAGGAAGTCAAAT	
		-----AGGGTGGCCTTGGCAAAGAGGAAGTCAAAT	
HGRA4sv.cds	(101)	101	150
SEQ ID NO:23	(32)	CTGGAACCAAGGGGTCCCAGCCCATGTCCCCCTCTGATTTCTAGACAAA	
		CTGGAACCAAGGGGTCCCAGCCCATGTCCCCCTCTGATTTCTAGACAAA	
HGRA4sv.cds	(151)	151	200
SEQ ID NO:23	(82)	CTTATGGGGCGAACATCTGGATATGATGCCAGGATTCGGCCCCAATTTTAA	
		CTTATGGGGCGAACATCTGGATATGATGCCAGGATTCGGCCCCAATTTTAA	
HGRA4sv.cds	(201)	201	250
SEQ ID NO:23	(132)	AGGCCACCCGTGAACGTGACCTGCAACATCTTCATCAACAGTTTCAGCT	
		AGGCCACCCGTGAACGTGACCTGCAACATCTTCATCAACAGTTTCAGCT	
HGRA4sv.cds	(251)	251	300
SEQ ID NO:23	(182)	CCGTCACCAAGACCACAATGGACTACCGGGTGAATGTCTTCTTGCGGCAA	
		CCATCACCAAGACCACAATGGACTACCGGGTGAATGTCTTCTTGCGGCAA	
HGRA4sv.cds	(301)	301	350
SEQ ID NO:23	(232)	CAGTGGAAATGACCCACGCCCTGTCTACCGAGAATATCCTGATGACTCTCT	
		CAGTGGAAATGACCCACGCCCTGTCTACCGAGAATATCCTGATGACTCTCT	
HGRA4sv.cds	(351)	351	400
SEQ ID NO:23	(282)	GGACCTCGATCCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCT	
		GGACCTCGATCCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCT	
HGRA4sv.cds	(401)	401	450
SEQ ID NO:23	(332)	TTGCTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGGACAACAAG	
		TTGCTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGGACAACAAG	
HGRA4sv.cds	(451)	451	500
SEQ ID NO:23	(382)	TTACTGCGCATCTTCAAGAATGGGAATGTGCTGTACAGCATCAGGCTGAC	
		TTACTGCGCATCTTCAAGAATGGGAATGTGCTGTACAGCATCAGGCTGAC	
HGRA4sv.cds	(501)	501	550
SEQ ID NO:23	(432)	CCTCATTTTGTCTGCTGATGGACCTCAAGAACTTCCCCATGGACATCC	
		CCTCATTTTGTCTGCTGATGGACCTCAAGAACTTCCCCATGGACATCC	
HGRA4sv.cds	(551)	551	600
SEQ ID NO:23	(482)	AGACGTGCACGATGCAGCTTGAGAGCTCATCCATACTCTGCAGCCCTCTG	
		AGACGTGCACGATGCAGCTTGAGAGCT-----	
HGRA4sv.cds	(601)	601	650
SEQ ID NO:23	(509)	CCATCTCTGTCACTTTCAGTTGGCTACACCATGAAAGACCTCGTGTTTGA	
		-----TTGGCTACACCATGAAAGACCTCGTGTTTGA	
HGRA4sv.cds	(651)	651	700
SEQ ID NO:23	(540)	GTGGCTGGAAGATGCTCCTGCTGTCCAAGTGGCTGAGGGGCTGACTCTGC	
		GTGGCTGGAAGATGCTCCTGCTGTCCAAGTGGCTGAGGGGCTGACTCTGC	
		701	750

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HGRA4sv.cds	(701)	CCCAAGTTTATCTTGCGGGATGAGAAGGATCTAGGCTGTTGTACCAAGCAC	
SEQ ID NO:23	(590)	CCCAAGTTTATCTTGCGGGATGAGAAGGATCTAGGCTGTTGTACCAAGCAC	
		751	800
HGRA4sv.cds	(751)	TACAACACAGGGAAATTCACCTGCATCGAGGTAAAGTTTCACCTGGAACG	
SEQ ID NO:23	(640)	TACAACACAGGGAAATTCACCTGCATCGAGGTAAAGTTTCACCTGGAACG	
		801	850
HGRA4sv.cds	(801)	GCAGATGGGCTACTATCTGATTCAGATGTACATCCCCAGCCTACTCATCG	
SEQ ID NO:23	(690)	GCAGATGGGCTACTATCTGATTCAGATGTACATCCCCAGCCTACTCATCG	
		851	900
HGRA4sv.cds	(851)	TCATCCTGTCCTGGGTCTCCTTCTGGATCAACATGGATGCTGCCCCCTGCC	
SEQ ID NO:23	(740)	TCATCCTGTCCTGGGTCTCCTTCTGGATCAACATGGATGCTGCCCCCTGCC	
		901	950
HGRA4sv.cds	(901)	CGTGTGGGCCTGGGCATCACCACCGTGCTCACCATGACCACCCAGAGCTC	
SEQ ID NO:23	(790)	CGTGTGGGCCTGGGCATCACCACCGTGCTCACCATGACCACCCAGAGCTC	
		951	1000
HGRA4sv.cds	(951)	TGGCTCCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGACA	
SEQ ID NO:23	(840)	TGGCTCCCGGGCCTCTTTGCCTAAGGTG-----	
		1001	1050
HGRA4sv.cds	(1001)	TCTGGATGGCTGTGTGTCTGCTCTTTGTGTTGCTGCCTTGCTGGAGTAT	
SEQ ID NO:23	(868)	-----	
		1051	1100
HGRA4sv.cds	(1051)	GCTGCCATAAATTTTGTCTCGTCAGCATAAAGAATTCATACGACTTCG	
SEQ ID NO:23	(868)	-----	
		1101	1150
HGRA4sv.cds	(1101)	AAGAAGGCAGAGGCGCCAACGCTTGGAGGAAGATATCATCCAAGAAAGTC	
SEQ ID NO:23	(868)	-----	
		1151	1200
HGRA4sv.cds	(1151)	GTTTCTATTTCCGTGGCTATGGCTTGGGCCACTGCCTGCAGGCAAGAGAT	
SEQ ID NO:23	(868)	-----	
		1201	1250
HGRA4sv.cds	(1201)	GGAGGTCCAATGGAAGGTTCTGGCATTATAGTCCCCAACCTCCAGCCCC	
SEQ ID NO:23	(868)	-----	
		1251	1293
HGRA4sv.cds	(1251)	TCTTCTAAGGGAAGGAGAAACCACGCGAAACTCTACGTGGAC	
SEQ ID NO:23	(868)	-----	

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HGRA4sv.cds	(1)	1	50
SEQ ID NO:55	(1)	ATGACAACCTCTTGTTCCTGCAACCCTCTCCTTCCTTCTTCTCTGGACCC	

HGRA4sv.cds	(51)	51	100
SEQ ID NO:55	(1)	GCCAGGGCAGGTCCCTCCTCAGGGTGGCCTTGGCAAAGAGGAAGTCAAAT	

HGRA4sv.cds	(101)	101	150
SEQ ID NO:55	(1)	CTGGAACCAAGGGGTCCCAGCCCATGTCCCCCTCTGATTTCTAGACAAA	

HGRA4sv.cds	(151)	151	200
SEQ ID NO:55	(1)	CTTATGGGGCGAACATCTGGATATGATGCCAGGATTCGGCCCAATTTTAA	

HGRA4sv.cds	(201)	201	250
SEQ ID NO:55	(1)	AGGCCACCCGTGAACGTGACCTGCAACATCTTCATCAACAGTTTCAGCT	

HGRA4sv.cds	(251)	251	300
SEQ ID NO:55	(1)	CCGTCACCAAGACCACAATGGACTACCGGGTGAATGTCTTCTTGCGGCAA	

HGRA4sv.cds	(301)	301	350
SEQ ID NO:55	(1)	CAGTGAATGACCCACGCCTGTCCTACCGAGAATATCCTGATGACTCTCT	

HGRA4sv.cds	(351)	351	400
SEQ ID NO:55	(1)	GGACCTCGATCCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCT	

HGRA4sv.cds	(401)	401	450
SEQ ID NO:55	(1)	TTGCTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGGACAACAAG	

HGRA4sv.cds	(451)	451	500
SEQ ID NO:55	(1)	TTACTGCGCATCTTCAAGAATGGGAATGTGCTGTACAGCATCAGGCTGAC	

HGRA4sv.cds	(501)	501	550
SEQ ID NO:55	(1)	CCTCATTTTGTCTCTGCCTGATGGACCTCAAGAACTTCCCCATGGACATCC	

HGRA4sv.cds	(551)	551	600
SEQ ID NO:55	(1)	AGACGTGCACGATGCAGCTTGAGAGCTCATCCATACTCTGCAGCCCTCTG	

HGRA4sv.cds	(601)	601	650
SEQ ID NO:55	(1)	CCATCTCTGTCACTTTTCAGTTGGCTACACCATGAAAGACCTCGTGTGTTGA	

HGRA4sv.cds	(651)	651	700
SEQ ID NO:55	(1)	GTGGCTGGAAGATGCTCCTGCTGTCCAAGTGGCTGAGGGGCTGACTCTGC	

		701	750

HGRA4sv.cds	(701)	CCCAAGTTTATCTTGC	GGGATGAGAAGGATCTAGGCTGTTGTACCAAGCAC
SEQ ID NO:55	(1)	-----	
		751	800
HGRA4sv.cds	(751)	TACAACACAGGGAAATT	CACCTGCATCGAGGTAAAGTTTACCTGGAACG
SEQ ID NO:55	(1)	-----	
		801	850
HGRA4sv.cds	(801)	GCAGATGGGCTACTATCTGATT	CAGATGTACATCCCCAGCCTACTCATCG
SEQ ID NO:55	(1)	-----	
		851	900
HGRA4sv.cds	(851)	TCATCCTGTCCTGGGTCTCCTTCTGGATCAACATGGATGCTGCCCCCTGCC	
SEQ ID NO:55	(1)	-----	
		901	950
HGRA4sv.cds	(901)	CGTGTGGGCTGGGCATCACCACCGTGCTCACCATGACCACCCAGAGCTC	
SEQ ID NO:55	(1)	-----	
		951	1000
HGRA4sv.cds	(951)	TGGCTCCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGACA	
SEQ ID NO:55	(1)	-----	
		1001	1050
HGRA4sv.cds	(1001)	TCTGGATGGCTGTGTGTCTGCTCTTTGTGTTTCGCTGCCTTGCTGGAGTAT	
SEQ ID NO:55	(1)	---GGATGGCTGTGTGTCTGCTCTTTGTGTTTCGCTGCCTTGCTGGAGTAT	
		1051	1100
HGRA4sv.cds	(1051)	GCTGCCATAAATTTTGTCTCGTCAGCATAAAGAATTCATACGACTTCG	
SEQ ID NO:55	(48)	GCTGCCATAAATTTTGTCTCGTCAGCATAAAGAATTCATACGACTTCG	
		1101	1150
HGRA4sv.cds	(1101)	AAGAAGGCAGAGGCGCCAACGCTTGGAGGAAGATATCATCCAAGAAAGTC	
SEQ ID NO:55	(98)	AAGAAGGCAGAGGCGCCAACGCTTGGAGGAAGATATCATCCAAGAAAGTC	
		1151	1200
HGRA4sv.cds	(1151)	GTTTCTATTTCCGTGGCTATGGCTTGGGCCACTGCCTGCAGGCAAGAGAT	
SEQ ID NO:55	(148)	GTTTCTATTTCCGTGGCTATGGCTTGGGCCACTGCCTGCAGGCAAGAGAT	
		1201	1250
HGRA4sv.cds	(1201)	GGAGGTCCAATGGAAGGTTCTGGCATTATAGTCCCCAACCTCCAGCCCC	
SEQ ID NO:55	(198)	GGAGGTCCAATGGAAGGTTCTGGCATTATAGTCCCCAACCTCCAGCCCC	
		1251	1300
HGRA4sv.cds	(1251)	TCTTCTAAGGGAAGGAGAAACCACGCGGAAACTCTACGTGGAC	-----
SEQ ID NO:55	(248)	TCTTCTAAGGGAAGGAGAAACCACGCGGAAACTCTACGTGGACTGAGCCA	
		1301	1350
HGRA4sv.cds	(1294)	-----	
SEQ ID NO:55	(298)	AGAGAATTGACACCATCTCCCGGGCTGTCTTCCCTTTCACTTTCCTCATC	
		1351	1400
HGRA4sv.cds	(1294)	-----	
SEQ ID NO:55	(348)	TTCAATATCTTCTACTGGGTTGTCTATAAAGTGCTATGGTCAGAAAGNTAN	

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		1401		1450
HGRA4sv.cds	(1294)	-----		
SEQ ID NO:55	(398)	CCACCAGGCTCTGTGAATAGGGTGGGAGCTATAGAGTCCTGCTGCTGGCC		
		1451		1500
HGRA4sv.cds	(1294)	-----		
SEQ ID NO:55	(448)	TCCTGCTTCCTCCTGGGTGGGNTTCTCCCTCAGTTAGACTCCATTAGGG		
		1501		1550
HGRA4sv.cds	(1294)	-----		
SEQ ID NO:55	(498)	GTTTGGACAGTTCCTTCCTGATCTCCANTCAGAACTTCATCTACCAGTN		
		1551	1575	
HGRA4sv.cds	(1294)	-----		
SEQ ID NO:55	(548)	CCAAAGCTATGTGGGCCTATATTGC		



		1	50
HGRA4sv	(1)	MTTLVPATLSFLLLWTLPGQVLL	RVALAKEEVKSGTKGSQPMSPSDFLDK
SEQ ID NO:41	(1)	-----	-----
SEQ ID NO:50	(1)	-----	RVALAKEEVKSGTKGSQPMSPSDFLDK
		51	100
HGRA4sv	(51)	LMGRTSGYDARIRPNFKGPPVNVTCNIFINSFSS	TKTTMDYRVNVFLRQ
SEQ ID NO:41	(1)	-----	-----
SEQ ID NO:50	(28)	LMGRTSGYDARIRPNFKGPPVNVTCNIFINSFSS	TKTTMDYRVNVFLRQ
		101	150
HGRA4sv	(101)	QWNDPRLSYREYPDDSLDLDP SMLDSIWKPDLFFANEKGANFHEVTTDNK	
SEQ ID NO:41	(1)	-----	-----
SEQ ID NO:50	(78)	QWNDPRLSYREYPDDSLDLDP SMLDSIWKPDLFFANEKGANFHEVTTDNK	
		151	200
HGRA4sv	(151)	LLRIFKNGNVLYSIRLTLILSCLMDLKNFPMDIQTCTMQLES	SSILCSPL
SEQ ID NO:41	(1)	-----	-----
SEQ ID NO:50	(128)	LLRIFKNGNVLYSIRLTLILSCLMDLKNFPMDIQTCTMQLES	-----
		201	250
HGRA4sv	(201)	PSLSLSV	GYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDLGCCTKH
SEQ ID NO:41	(1)	-----	-----
SEQ ID NO:50	(170)	-----	GYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDLGCCTKH
		251	300
HGRA4sv	(251)	YNTGKFTCIEVKFHLE RQMGGYLIQMYIPSL	LIVILSWVSFWINMDAAPA
SEQ ID NO:41	(1)	-----	-----
SEQ ID NO:50	(214)	YNTGKFTCIEVKFHLE RQMGGYLIQMYIPSL	LIVILSWVSFWINMDAAPA
		301	350
HGRA4sv	(301)	RVGLGITTVLMTTQSSGSRASLPKVS	YKAIWIWMAVCLLFVFAALLEY
SEQ ID NO:41	(1)	-----	VS YKAIWIWMAVCLLFVFAALLEY
SEQ ID NO:50	(264)	RVGLGITTVLMTTQSSGSRASLPK	-----
		351	400
HGRA4sv	(351)	AAINFVSRQHKEFIRLRRRQRQRLEEDI	IQESRFYFRGYGLGHCLQARD
SEQ ID NO:41	(26)	AAINFVSRQHKEFIRLRRRQRQRLEEDI	IQESRFYFRGYGLGHCLQARD
SEQ ID NO:50	(290)	-----	-----
		401	450
HGRA4sv	(401)	GGPMEGSGIYSPQPPAPLLREGETTRKLYD	-----
SEQ ID NO:41	(76)	GGPMEGSGIYSPQPPAPLLREGETTRKLYD	AKRIDTISR AVFPFTFLIF
SEQ ID NO:50	(290)	-----	-----
		451	468
HGRA4sv	(432)	-----	-----
SEQ ID NO:41	(126)	NIFYWVYKVLWSEDIHQ	
SEQ ID NO:50	(290)	-----	-----

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HGRA4sv.cds	(1)	1	50
SEQ ID NO:14	(1)	ATGACAACCTCTTGTTTCCTGCAACCCTCTCCTTCCTTCTTCTCTGGACCCT	

HGRA4sv.cds	(51)	51	100
SEQ ID NO:14	(1)	GCCAGGGCAGGTCTCCTCAGGGTGGCCTTGGCAAAAGAGGAAGTCAAAT	

HGRA4sv.cds	(101)	101	150
SEQ ID NO:14	(1)	CTGGAACCAAGGGGTCCCAGCCCATGTCCCCCTCTGATTTCCTAGACAAA	

HGRA4sv.cds	(151)	151	200
SEQ ID NO:14	(1)	CTTATGGGGCGAACATCTGGATATGATGCCAGGATTCGGCCCAATTTTAA	

HGRA4sv.cds	(201)	201	250
SEQ ID NO:14	(1)	AGGCCCACCCGTGAACGTGACCTGCAACATCTTCATCAACAGTTTCAGCT	

HGRA4sv.cds	(251)	251	300
SEQ ID NO:14	(1)	CCGTCACCAAGACCACAATGGACTACCGGGTGAATGTCTTCTTGC GGCAA	

HGRA4sv.cds	(301)	301	350
SEQ ID NO:14	(1)	CAGTGGAATGACCCACGCCTGTCCTACCGAGAATATCCTGATGACTCTCT	

HGRA4sv.cds	(351)	351	400
SEQ ID NO:14	(1)	GGACCTCGATCCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCT	

HGRA4sv.cds	(401)	401	450
SEQ ID NO:14	(1)	TTGCTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGGACAACAAG	

HGRA4sv.cds	(451)	451	500
SEQ ID NO:14	(1)	TTACTGCGCATCTTCAAGAATGGGAATGTGCTGTACAGCATCAGGCTGAC	

HGRA4sv.cds	(501)	501	550
SEQ ID NO:14	(1)	CCTCATTTTGTCTGCTGATGGACCTCAAGAACTTCCCCATGGACATCC	

HGRA4sv.cds	(551)	551	600
SEQ ID NO:14	(1)	AGACGTGCACGATGCAGCTTGAGAGCTCATCCATACTCTGCAGCCCTCTG	

HGRA4sv.cds	(601)	601	650
SEQ ID NO:14	(1)	CCATCTCTGTCACTTTCAGTTGGCTACACCATGAAAGACCTCGTGTTTGA	

HGRA4sv.cds	(651)	651	700
SEQ ID NO:14	(1)	GTGGCTGGAAGATGCTCCTGCTGTCCAAGTGGCTGAGGGGCTGACTCTGC	

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HGRA4sv.cds	(701)	CCCAAGTTTATCTTGC	GGGATGAGAAGGATCTAGGCTGTTGTACCAAGCAC	
SEQ ID NO:14	(1)	-----		
		751		800
HGRA4sv.cds	(751)	TACAACACAGGGAAATTCACCTGCATCGAGGTAAAGTTTCACCTGGAACG		
SEQ ID NO:14	(1)	-----		
		801		850
HGRA4sv.cds	(801)	GCAGATGGGCTACTATCTGATTCAGATGTACATCCCCAGCCTACTCATCG		
SEQ ID NO:14	(1)	-----		
		851		900
HGRA4sv.cds	(851)	TCATCCTGTCCTGGGTCTCCTTCTGGATCAACATGGATGCTGCCCCCTGCC		
SEQ ID NO:14	(1)	-----		
		901		950
HGRA4sv.cds	(901)	CGTGTGGGCCTGGGCATCACCACCGTGCTCACCATGACCACCCAGAGCTC		
SEQ ID NO:14	(1)	-----		
		951		1000
HGRA4sv.cds	(951)	TGGCTCCCGGGCCTCTTTGCCTAAG	GTGTCCTACGTGAAGGCAATCGACA	
SEQ ID NO:14	(1)	-----	GTGTCCTACGTGAAGGCAATCGACA	
		1001		1050
HGRA4sv.cds	(1001)	TCTGGATGGCTGTGTGCTGCTCTTTGTGTTGCTGCCTTGCTGGAGTAT		
SEQ ID NO:14	(26)	TCTGGATGGCTGTGTGCTGCTCTTTGTGTTGCTGCCTTGCTGGAGTAT		
		1051		1100
HGRA4sv.cds	(1051)	GCTGCCATAAAATTTGTTTCTCGTCAGCATAAAGAATTCATACGACTTCG		
SEQ ID NO:14	(76)	GCTGCCATAAAATTTGTTTCTCGTCAGCATAAAGAATTCATACGACTTCG		
		1101		1150
HGRA4sv.cds	(1101)	AAGAAGGCAGAGGCGCCAACGCTTGGAGGAAGATATCATCCAAGAAAGTC		
SEQ ID NO:14	(126)	AAGAAGGCAGAGGCGCCAACGCTTGGAGGAAGATATCATCCAAGAAAGTC		
		1151		1200
HGRA4sv.cds	(1151)	GTTTCTATTTCCGTGGCTATGGCTTGGGCCACTGCCTGCAGGCAAGAGAT		
SEQ ID NO:14	(176)	GTTTCTATTTCCGTGGCTATGGCTTGGGCCACTGCCTGCAGGCAAGAGAT		
		1201		1250
HGRA4sv.cds	(1201)	GGAGGTCCAATGGAAGGTTCTGGCATTTATAGTCCCCAACCTCCAGCCCC		
SEQ ID NO:14	(226)	GGAGGTCCAATGGAAGGTTCTGGCATTTATAGTCCCCAACCTCCAGCCCC		
		1251		1300
HGRA4sv.cds	(1251)	TCTTCTAAGGGAAGGAGAAACCACGCGGAAACTCTACGTGGAC	-----	
SEQ ID NO:14	(276)	TCTTCTAAGGGAAGGAGAAACCACGCGGAAACTCTACGTGGAC	-----	TGAGCCA
		1301		1350
HGRA4sv.cds	(1294)	-----		
SEQ ID NO:14	(326)	AGAGAATTGACACCATCTCCCGGGCTGTCTTCCCTTTCACTTTCTCATC		
		1351		1400
HGRA4sv.cds	(1294)	-----		
SEQ ID NO:14	(376)	TTCAATATCTTCTACTGGGTTGTCTATAAAGTGCTATGGTCAGAAGATAT		

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HGRA4sv.cds (1294) -----
SEQ ID NO:14 (426) CCACCAG